

SHEEP SYMPOSIUM

Emerging Genetic Technology to Improve Sheep Production

27 A genetic map of the ovine genome. C. W. Beattie^{1*}, B. A. Freking¹, M. G. de Gortari¹, K. G. Dodds², S. M. Kappes¹, J. W. Keele¹, R. T. Stone¹, K. A. Leymaster¹, and A. M. Crawford², ¹U.S. Meat Animal Research Center, Clay Center, NE and ²AgResearch Molecular Biology Unit, University of Otago, Dunedin, New Zealand.

A genetic map of *Ovis aries* (haploid N=27) was developed with 514 microsatellite (ms) loci in 26 autosomal linkage groups spanning 3022.3 centimorgans (cM; sex-average) and 102.9 cM (female-specific) of the X chromosome. Genomic conservation among Bovidae allowed the extensive use of ms developed in bovine (397/500 ms, 79.4%) in sheep. Individual linkage groups averaged 19 markers (range 8-48) and 115.8 cM (range 49.0-294.5 cM). The average interval (n=487) between adjacent linkage markers was 6.4 cM, with 55.5% of the intervals < 5 cM and only 3.8% of the intervals > 20 cM. Twenty of the 26 autosomes are oriented with respect to the centromere, either directly in sheep or indirectly through orientation on the homologous bovine chromosome. Sixty-six percent (348/500) of the ms on the current sheep map are common on the USDA-ARS cattle map. The common markers span 2866 cM (sex-averaged) in sheep and 2817 cM in cattle or approximately 95% of each genome. Marker order within a linkage group was consistent between the two species with limited exceptions. The previously reported translocation of the telomeric end of BTA9 to BTA14 in sheep (OOV9) (Crawford et al., 1994) is represented by a 15 cM region containing five common markers. The other exceptions involved five independent markers (1.5% of the 348 common markers) from different linkage groups that did not map to the expected homologue linkage group. The high degree of genomic conservation between sheep and cattle will allow us to simultaneously use conserved linkage and physical mapping information while searching for quantitative trait loci (QTL) in both species.

Key Words: Sheep, Genetic, Map

28 Marker Assisted Selection of Sheep. M. D. Bishop, ABS Global, Inc., DeForest, Wisconsin.

Genetic linkage maps for sheep chromosomes ordering several hundred microsatellite markers and a few genes by meiotic recombination have recently been developed. The derivation of these maps was accomplished in a similar manner as those for cattle and for pigs using families of animals (reference families) constructed to maximize heterozygosity in some cases and for trait specific segregation (resource families) in others. Several of the microsatellite markers used to form the backbone of the sheep linkage groups were derived from cattle maps. Now the task begins to utilize these maps in dissecting monogenic and polygenic traits to identify markers and genes for traits important to sheep producers. Information learned from mapping projects in other species will also aid the discovery of these important genomic regions and eventually lead to implementation of DNA based Marker-Assisted-Selection. Once genomic regions have been flanked with DNA markers the advantages of MAS can be exploited in breeding schemes aimed at fixing or optimizing trait variation, eliminating lethal or deleterious recessives from a population, introgressing genes from one population to another at a faster rate than that accomplished with traditional selection methods or identifying Mendelian sampling effects in animals being selected early in life before trait expression which have inherited genomic intervals containing Economic Trait Loci. There are several methods which can be used depending on the type of trait and the DNA resources available to initially identify the chromosomal region(s) containing the gene(s) of interest leading to more comprehensive methods for fine mapping the chromosomal region and discovery of tightly linked markers which can be used in MAS. Once a set of markers with sufficient informativeness and low levels of recombination have been linked to ETL (monogenic or polygenic) they can be used in linkage haplotyping to follow the inheritance of ETL containing chromosomal region(s) from parent to offspring increasing selection intensity and early prediction of progeny expressed phenotype. Factors limiting the exploitation of MAS in farm animal species are available populations of animals from which the investigator has a reasonable chance of finding the chromosomal region of interest, resources for completing the task, phenotypic data that clearly relates the trait variance of interest with the animals typed and clear economic objectives for utilizing the markers once identified.

Key Words: Sheep, Mapping, Marker-Assisted-Selection

29 Multitrait Index Selection of Sheep. G. D. Snowder, USDA,ARS, U.S. Sheep Experiment Station, Dubois, ID.

Sheep are dual purpose animals producing meat and fiber. Simultaneous genetic improvement of meat and fiber can occur by using multitrait selection procedures to develop a total score of genetic merit for each animal. An animal's total score or index is derived by summing the animal's estimated breeding values for each trait which are weighted by the trait's economic value. The usefulness of multitrait selection indices is dependent on reliable genetic and phenotypic parameters (heritability estimates, repeatabilities, and genetic and phenotypic correlations) and economic weights. Often the genetic and phenotypic parameters for major production traits are known; but less reliable estimates may exist for such traits as feed conversion and lamb survival. Economic weights are the most difficult values to derive because they vary across production systems and most predict future economic conditions. Ideally, an index considers all costs and revenues associated with a unit change in each trait. In reality, not every trait has a definite economic value. Relative economic values are influenced by many factors including: predation losses, age and/or weight of weaned lamb, private vs public grazing, diseases, grain and roughage costs, lamb prices, etc. If all of these factors were to be considered, the result would be development of several, if not many, multitrait indices for generalized types of production systems. Also, breeding objectives differ among breeds. Selection objectives for terminal sire breeds will certainly differ from those for maternal breeds. Determination of which traits to include in an index should be based on economic importance, benefits of measurement, and correlation with other traits. The National Sheep Improvement Program provides a way to introduce multitrait index selection to breeders. The first multitrait indices should be reliable, practical and easily understood to enhance initial public acceptance.

Key Words: Selection, Sheep, Breeding

30 Ovine disease and breeding for parasite resistance. R. R. Woolaston* and S. J. Eady, CSIRO Division of Animal Production, Armidale.

The distribution of sheep production is frequently governed by disease prevalence and some diseases can restrict local and international trade. The best methods for prevention and control are cheap, effective and sustainable. Control methods for most parasites of sheep rely on chemicals. Such methods are usually cost effective in the short term but it seems inevitable that parasites develop resistance to anti-parasitic chemicals. This problem is at its worst with gastro-intestinal nematodes. Fortunately there is genetic variation between sheep in resistance to parasites, both between breeds and within flocks, and workers in several countries are investigating ways of harnessing this variation. Faecal worm egg count (FEC) is a simple and useful indicator of worm burden, is moderately heritable (20-30%) and so is a good selection criterion for identifying resistant sheep. Trials have shown that breeding can be more effective in reducing infective larvae on pasture than other control measures, including strategic anthelmintic use. Many ram breeders in Australia and New Zealand are improving the resistance of their flocks through measuring FEC. Other selection criteria with promise include faecal antigens, serum antibodies, and where blood-sucking parasites are prevalent, packed cell volume. The relationships between the ability of sheep to reduce worm numbers, to tolerate the effects of worms and to maintain production under worm challenge are complex and require further research. Genetic markers offer potential when selecting for disease resistance but less so for worm resistance because worms are widespread and FEC is moderately heritable, easy to measure and continuously distributed. Nevertheless, understanding the genetic basis for resistance is worthwhile as it may lead to the development of other novel control measures. Genetic markers may also be particularly useful when introgressing desirable genes from relatively unimproved, yet resistant breeds.

Key Words: Sheep, Parasites, Breeding